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==============================================================
Sequence Listing was accepted.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Keisha Douglas
Timestamp: [year=2008; month=10; day=23; hr=16; min=48; sec=47; ms=752;
]
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                   Validated By CRFValidator v 1.0.3

        Application No:        10573601            Version No:        2.1


                        Input Set:


                        Output Set:



                   Started:   2008-10-23 16:46:51.257
                  Finished:   2008-10-23 16:46:55.642
                   Elapsed:   0 hr(s) 0 min(s) 4 sec(s) 385 ms
           Total Warnings:    4
             Total Errors:    20
      No. of SeqIDs Defined:  6
          Actual SeqID Count: 6


   Error code      Error Description


W  213         Artificial or Unknown found in <213>  in SEQ ID (3)

E  257         Invalid sequence data feature in <221>  in SEQ ID (3)

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E  257         Invalid sequence data feature in <221>  in SEQ ID (3)

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E  257         Invalid sequence data feature in <221>  in SEQ ID (5)

W  213         Artificial or Unknown found in <213>  in SEQ ID (6)

E  257         Invalid sequence data feature in <221>  in SEQ ID (6)
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Input Set:

Output Set:

Started:	2008-10-23 16:46:51.257
Finished:	2008-10-23 16:46:55.642
Elapsed:	0 hr(s) 0 min(s) 4 sec(s) 385 ms
Total Warnings:	4
Total Errors:	20
No. of SeqIDs Defined:	6
Actual SeqID Count:	6

Error code	Error Description
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E 257	Invalid sequence data feature in <221> in SEQ ID (6)
E 257	Invalid sequence data feature in <221> in SEQ ID (6)
E 257	Invalid sequence data feature in <221> in SEQ ID (6) This error has occured more than 20 times, will not be displayed

<110> HANSSON, HANS-ARNE
       JENNISCHE, EVA
       LANGE, STEFAN
       LON-NROTH, IVAR
       ERIKSSON, PETER
       PERSSON, ANDERS

<120> NOVEL USE OF ANTISECRETORY FACTOR

<130> 1003301-000258

<140> 10/573,601
<141> 2006-08-11

<150> PCT/SE04/001369
<151> 2004-09-24

<150> GB 0322645.3
<151> 2003-09-26

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<213> Homo sapiens

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Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp Ala
             20   25   30

Val Asn Ile Val Cys His Ser Lys Thr Arg Ser Asn Pro Glu Asn Asn
         35   40   45

Val Gly Leu Ile Thr Leu Ala Asn Asp Cys Glu Val Leu Thr Thr Leu
     50   55   60

Thr Pro Asp Thr Gly Arg Ile Leu Ser Lys Leu His Thr Val Gln Pro
 65   70   75   80

Lys Gly Lys Ile Thr Phe Cys Thr Gly Ile Arg Val Ala His Leu Ala
                 85   90   95

Leu Lys His Arg Gln Gly Lys Asn His Lys Met Arg Ile Ile Ala Phe
                100   105   110

Val Gly Ser Pro Val Glu Asp Asn Glu Lys Asp Leu Val Lys Leu Ala
            115   120   125

Lys Arg Leu Lys Lys Glu Lys Val Asn Val Asp Ile Ile Asn Phe Gly

Glu Glu Glu Val Asn Thr Glu Lys Leu Thr Ala Phe Val Asn Thr Leu
145   150   155   160

Asn Gly Lys Asp Gly Thr Gly Ser His Leu Val Thr Val Pro Pro Gly
                    165   170   175

Pro Ser Leu Ala Asp Ala Leu Ile Ser Ser Pro Ile Leu Ala Gly Glu
                180   185   190

Gly Gly Ala Met Leu Gly Leu Gly Ala Ser Asp Phe Glu Phe Gly Val
                195   200   205

Asp Pro Ser Ala Asp Pro Glu Leu Ala Leu Ala Leu Arg Val Ser Met
                210   215   220

Glu Glu Gln Arg His Ala Gly Gly Gly Ala Arg Arg Ala Ala Arg Ala
225   230   235   240

Ser Ala Ala Glu Ala Gly Ile Ala Thr Thr Gly Thr Glu Asp Ser Asp
                245   250   255

Asp Ala Leu Leu Lys Met Thr Ile Ser Gln Gln Glu Phe Gly Arg Thr
                260   265   270

Gly Leu Pro Asp Leu Ser Ser Ser Thr Glu Glu Glu Glu Ile Ala Tyr
                275   280   285

Ala Met Gln Met Ser Leu Gln Gly Ala Glu Phe Gly Gln Ala Glu Ser
                290   295   300

Ala Asp Ile Asp Ala Ser Ser Ala Met Asp Thr Ser Glu Pro Ala Lys
305   310   315   320

Glu Glu Asp Asp Tyr Asp Val Met Gln Asp Pro Glu Phe Leu Gln Ser
                325   330   335

Val Leu Glu Asn Leu Pro Gly Val Asp Pro Asn Asn Glu Ala Ile Arg
                340   345   350

Asn Ala Met Gly Ser Leu Pro Pro Arg Pro Pro Arg Thr Ala Arg Arg
                355   360   365

Thr Arg Arg Arg Lys Thr Arg Ser Glu Thr Gly Gly Lys Gly
370   375   380

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   Met Val Leu Glu Ser Thr Met Val Cys Val Asp Asn Ser Glu Tyr
     1   5   10   15

atg cgg aat gga gac ttc tta ccc acc agg ctg cag gcc cag cag gat   155
Met Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp
                20   25   30

gct gtc aac ata gtt tgt cat tca aag acc cgc agc aac cct gag aac   203
Ala Val Asn Ile Val Cys His Ser Lys Thr Arg Ser Asn Pro Glu Asn
            35   40   45

aac gtg ggc ctt atc aca ctg gct aat gac tgt gaa gtg ctg acc aca   251
Asn Val Gly Leu Ile Thr Leu Ala Asn Asp Cys Glu Val Leu Thr Thr
        50   55   60

ctc acc cca gac act ggc cgt atc ctg tcc aag cta cat act gtc caa   299
Leu Thr Pro Asp Thr Gly Arg Ile Leu Ser Lys Leu His Thr Val Gln
    65   70   75

ccc aag ggc aag atc acc ttc tgc acg ggc atc cgc gtg gcc cat ctg   347
Pro Lys Gly Lys Ile Thr Phe Cys Thr Gly Ile Arg Val Ala His Leu
 80   85   90   95

gct ctg aag cac cga caa ggc aag aat cac aag atg cgc atc att gcc   395
Ala Leu Lys His Arg Gln Gly Lys Asn His Lys Met Arg Ile Ile Ala
                100   105   110

ttt gtg gga agc cca gtg gag gac aat gag aag gat ctg gtg aaa ctg   443
Phe Val Gly Ser Pro Val Glu Asp Asn Glu Lys Asp Leu Val Lys Leu
                115   120   125

gct aaa cgc ctc aag aag gag aaa gta aat gtt gac att atc aat ttt   491
Ala Lys Arg Leu Lys Lys Glu Lys Val Asn Val Asp Ile Ile Asn Phe
        130   135   140

ggg gaa gag gag gtg aac aca gaa aag ctg aca gcc ttt gta aac acg   539
Gly Glu Glu Glu Val Asn Thr Glu Lys Leu Thr Ala Phe Val Asn Thr
    145   150   155

ttg aat ggc aaa gat gga acc ggt tct cat ctg gtg aca gtg cct cct   587
Leu Asn Gly Lys Asp Gly Thr Gly Ser His Leu Val Thr Val Pro Pro
160   165   170   175

ggg ccc agt ttg gct gat gct ctc atc agt tct ccg att ttg gct ggt   635
Gly Pro Ser Leu Ala Asp Ala Leu Ile Ser Ser Pro Ile Leu Ala Gly
                180   185   190

gaa ggt ggt gcc atg ctg ggt ctt ggt gcc agt gac ttt gaa ttt gga   683
Glu Gly Gly Ala Met Leu Gly Leu Gly Ala Ser Asp Phe Glu Phe Gly
                195   200   205

gta gat ccc agt gct gat cct gag ctg gcc ttg gcc ctt cgt gta tct   731
Val Asp Pro Ser Ala Asp Pro Glu Leu Ala Leu Ala Leu Arg Val Ser

atg gaa gag cag cgg cac gca gga gga gga gcg cgg cgg gca gct cga   779
Met Glu Glu Gln Arg His Ala Gly Gly Gly Ala Arg Arg Ala Ala Arg
    225   230   235

gct tct gct gct gag gcc ggg att gct acg act ggg act gaa gac tca   827
Ala Ser Ala Ala Glu Ala Gly Ile Ala Thr Thr Gly Thr Glu Asp Ser
240   245   250   255

gac gat gcc ctg ctg aag atg acc atc agc cag caa gag ttt ggc cgc   875
Asp Asp Ala Leu Leu Lys Met Thr Ile Ser Gln Gln Glu Phe Gly Arg
                260   265   270

act ggg ctt cct gac cta agc agt agt act gag gaa gag gag att gct   923
Thr Gly Leu Pro Asp Leu Ser Ser Ser Thr Glu Glu Glu Glu Ile Ala
                275   280   285

tat gcc atg cag atg tcc ctg cag gga gca gag ttt ggc cag gcg gaa   971
Tyr Ala Met Gln Met Ser Leu Gln Gly Ala Glu Phe Gly Gln Ala Glu
            290   295   300

tca gca gac att gat gcc agc tca gct atg gac aca tct gag cca gcc   1019
Ser Ala Asp Ile Asp Ala Ser Ser Ala Met Asp Thr Ser Glu Pro Ala
    305   310   315

aag gag gag gat gat tac gac gtg atg cag gac ccc gag ttc ctt cag   1067
Lys Glu Glu Asp Asp Tyr Asp Val Met Gln Asp Pro Glu Phe Leu Gln
320   325   330   335

agt gtc cta gag aac ctc cca ggt gtg gat ccc aac aat gaa gcc att   1115
Ser Val Leu Glu Asn Leu Pro Gly Val Asp Pro Asn Asn Glu Ala Ile
                340   345   350

cga aat gct atg ggc tcc ctg cct ccc agg cca cca agg acg gca aga   1163
Arg Asn Ala Met Gly Ser Leu Pro Pro Arg Pro Pro Arg Thr Ala Arg
                355   360   365

agg aca aga agg agg aag aca aga agt gag act gga ggg aaa ggg   1208
Arg Thr Arg Arg Arg Lys Thr Arg Ser Glu Thr Gly Gly Lys Gly
        370   375   380

tagctgagtc tgcttagggg actgggaagc acggaatata gggttagatg tggttatctg 1268

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<211> 46
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<220>
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<222> (1)..(35)
<223> This region may or may not be present

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<222> (38)
<223> His, Arg or Lys

<220>
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              20   25   30

Val Asn Ile Val Cys Xaa Xaa Lys Xaa Arg Ser Asn Pro Glu
          35   40   45

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 1   5   10   15

Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp Ala
            20   25   30

Val Asn Ile Val Cys Xaa Xaa Lys Xaa Arg Ser Asn Pro Glu Asn Asn
        35   40   45

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<223> This region may or may not be present

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Met Val Leu Glu Ser Thr Met Val Cys Val Asp Asn Ser Glu Tyr Met
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Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp Ala
              20   25   30

Val Asn Ile Val Cys Xaa Xaa Lys Xaa Arg Ser Asn Pro Glu Asn Asn
          35   40   45

Val Gly Leu Ile Thr Leu Ala Asn Asp Cys Glu Val Leu Thr Thr Leu
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Thr Pro Asp Thr Gly Arg Ile Leu Ser Lys Leu His Thr Val Gln Pro
 65   70   75   80

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      amino acid sequence

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Met Val Leu Glu Ser Thr Met Val Cys Val Asp Asn Ser Glu Tyr Met
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Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp Ala
            20   25   30

Val Asn Ile Val Cys Xaa Xaa Lys Xaa Arg Ser Asn Pro Glu Asn Asn
            35   40   45

Val Gly Leu Ile Thr Leu Ala Asn Asp Cys Glu Val Leu Thr Thr Leu
        50   55   60

Thr Pro Asp Thr Gly Arg Ile Leu Ser Lys Leu His Thr Val Gln Pro
    65   70   75   80

Lys Gly Lys Ile Thr Phe Cys Thr Gly Ile Arg Val Ala His Leu Ala
                85   90   95

Leu Lys His Arg Gln Gly Lys Asn His Lys Met Arg Ile Ile Ala Phe
                100   105   110

Val Gly Ser Pro Val Glu Asp Asn Glu Lys Asp Leu Val Lys Leu Ala
        115   120   125

Lys Arg Leu Lys Lys Glu Lys Val Asn Val Asp Ile Ile Asn Phe Gly
    130   135   140

Glu Glu Glu Val Asn Thr Glu Lys Leu Thr Ala Phe Val Asn Thr Leu
145   150   155   160

Asn Gly Lys